Amendments to the claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of claims:

1. (Previously presented) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a first melanoma patient;

(b) amplifying mRNA transcripts encoded by a panel of marker genes from the nucleic acid from the SLN sample obtained from the first melanoma patient, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient; and

(d) predicting metastatic melanoma recurrence, metastatic melanoma-free survival, overall survival, or a combination thereof, for the first melanoma patient, wherein, as compared to the levels of mRNA transcripts encoded by the panel of marker genes in nucleic acid from an SLN sample obtained from a second melanoma patient, higher levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient indicate that the first melanoma patient has an increased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, a decreased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or a decreased probability of overall survival as compared to the probability of overall survival of the second melanoma patient, and lower levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient indicate that the first melanoma patient has a decreased probability of metastatic melanoma recurrence as compared to the probability of

metastatic melanoma recurrence of the second melanoma patient, an increased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or an increased probability of overall survival as compared to the probability of overall survival of the second melanoma patient.

2. (Previously presented) The method of claim 1 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3 and MART-1.

3. (Previously presented) The method of claim 2 wherein the panel comprises a first combination of MAGE-A3, GalNAcT, MART-1, and PAX3; or a second combination of MART-1, GalNAcT, and PAX3.

4. (Previously presented) The method of claim 1 wherein the nucleic acid is mRNA and the mRNA transcripts encoded by the panel of marker genes are amplified using real-time reverse transcriptase polymerase chain reaction (qRT-PCR).

5. (Previously presented) The method of claim 1 wherein the SLN sample is paraffin-embedded (PE) or frozen.

6. (Previously presented) The method of claim 1, wherein the SLN sample is histopathologically negative for melanoma cells.

7. (Previously presented) The method of claim 6, wherein histopathology of the SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

8-9. (Canceled)

10. (Previously presented) The method of claim 1, wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

11-33. (Canceled)

34. (Previously presented) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a blood sample obtained from a first melanoma patient;

(b) amplifying mRNA transcripts encoded by a panel of marker genes from the nucleic acid from the blood sample obtained from the first melanoma patient, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the blood sample obtained from the first melanoma patient; and

(d) predicting metastatic melanoma recurrence, metastatic melanoma-free survival, overall survival, or a combination thereof, for the first melanoma patient, wherein, as compared to the levels of mRNA transcripts encoded by the panel of marker genes in nucleic acid from a blood sample obtained from a second melanoma patient, higher levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the blood sample obtained from the first melanoma patient indicate that the first melanoma patient has an increased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, a decreased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or a decreased probability of overall survival as compared to the probability of overall survival of the second

melanoma patient, and lower levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the blood sample obtained from the first melanoma patient indicate that the first melanoma patient has a decreased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, an increased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or an increased probability of overall survival as compared to the probability of overall survival of the second melanoma patient.

35. (Previously presented) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a non-sentinel lymph node (NSLN) sample obtained from a first melanoma patient;

(b) amplifying mRNA transcripts encoded by a panel of marker genes from the nucleic acid from the NSLN sample obtained from the first melanoma patient, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the NSLN sample obtained from the first melanoma patient; and

(d) predicting metastatic melanoma recurrence, metastatic melanoma-free survival, overall survival, or a combination thereof, for the first melanoma patient, wherein, as compared to the levels of mRNA transcripts encoded by the panel of marker genes in nucleic acid from an NSLN sample obtained from a second melanoma patient, higher levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the NSLN sample obtained from the first melanoma patient indicate that the first melanoma patient has an increased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, a decreased probability of metastatic melanoma-free survival as compared to the probability of

metastatic melanoma-free survival of the second melanoma patient, or a decreased probability of overall survival as compared to the probability of overall survival of the second melanoma patient, and lower levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the NSLN sample obtained from the first melanoma patient indicate that the first melanoma patient has a decreased probability of metastatic melanoma recurrence as compared to the probability of metastatic melanoma recurrence of the second melanoma patient, an increased probability of metastatic melanoma-free survival as compared to the probability of metastatic melanoma-free survival of the second melanoma patient, or an increased probability of overall survival as compared to the probability of overall survival of the second melanoma patient.